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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/902,460

DATE: 12/10/2001
TIME: 11:25:51

Input Set : N:\Crf3\RULE60\09902460.txt
Output Set: N:\CRF3\12102001\I902460.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: FIDDES, J.C.
ABRAHAM, J.D.

(ii) TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH FACTOR ANALOG

(iii) NUMBER OF SEQUENCES: 69

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

ENTERED

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:
C--> (A) APPLICATION NUMBER: US/09/902,460
C--> (B) FILING DATE: 09-Jul-2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/098,628
(B) FILING DATE: 1998-06-16

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lehnhardt, Susan K
(B) REGISTRATION NUMBER: 33,943
(C) REFERENCE/DOCKET NUMBER: 21900-20089.10

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1969 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: Coding Sequence
(B) LOCATION: 970...1434
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AATTCATGCC TCTTTCTCTC CTTTTGTTGG TAGACGACTT CAGCCTCTGT CCTTTAATTT 60

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```
TAAAGTTTAT GCCCCACTTG TACCCCTCGT CTTTTGGTGA TTTAGAGATT TTCAAAGCCT    120
GCTCTGACAC AGACTCTTCC TTGGATTGCA ACTTCTCTAC TTTGGGGTGG AAACGGCTTC    180
TCCGTTTTGA AACGCTAGCG GGGAAAAAAT GGGGGAGAAA GTTGAGTTTA AACTTTTAAA    240
AGTTGAGTCA CGGCTGGTTG CGCACGAAAA GCCCCGCAGT GTGGAGAAAG CCTAAACGTG    300
GTTTGGGTGG TGCGGGGGTT GGGCGGGGGT GACTTTTGGG GGATAAGGGG CGGTGGAGCC    360
CAGGGAATGC CAAAGCCCTG CCGCGGCCTC CGACGCGCGC CCCCCGCCCC TCGCCTCTCC    420
CCCGCCCCCG ACTGAGGCCG GGCTCCCCGC CGGACTGATG TCGCGCGCTT GCGTGTTGTG    480
GCCGAAGCCG CCGAACTCAG AGGCCGGCCC CAGAAAACCC GAGCGAGTAG GGGGCGGCGC    540
GCAGGAGGGA GGAGAACTGG GGGCGCGGGA GGCTGGTGGG TGTGGGGGGT GGAGATGTAG    600
AAGATGTGAC GCCGCGGCCC GGCGGGTGCC AGATTAGCGG ACGGCTGCCC GCGGTTGCAA    660
CGGGATCCCG GGCGCTGCAG CTTGGGAGGC GGCTCTCCCC AGGCGGCGTC CGCGGAGACA    720
CCCATCTGTG AACCCCAGGT CCCGGGCCGC CGGCTCGCCG CGCACCAGGG GCCGGCGGAC    780
AGAAGAGCGG CCGAGCGGCT CGAGGCTGGG GGACCGCGGG CGCGGCCGCG CGCTGCCGGG    840
CGGGAGGCTG GGGGGCCGGG GCCGGGGCCG TGCCCGGAGC GGGTCGGAGG CCGGGGCCGG    900
GGCCGGGGGA CGGCGGCTCC CCGCGCGGCT CCAGCGGCTC GGGGATCCCG GCCGGGCCCC    960
GCAGGGACC ATG GCA GCC GGG AGC ATC ACC ACG CTG CCC GCC TTG CCC GAG   1011
            Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu
             1               5                  10
GAT GGC GGC AGC GGC GCC TTC CCG CCC GGC CAC TTC AAG GAC CCC AAG    1059
Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys
15                  20                  25                  30
CGG CTG TAC TGC AAA AAC GGG GGC TTC TTC CTG CGC ATC CAC CCC GAC    1107
Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp
                35                  40                  45
GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTA    1155
Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu
            50                  55                  60
CAA CTT CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT    1203
Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys
        65                  70                  75
 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT    1251
 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser
     80                  85                  90
 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT    1299
 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn
 95                  100                 105                 110
 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA    1347
 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala
                 115                 120                 125
 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG    1395
 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly
             130                 135                 140
 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG  1446
 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
         145                 150                 155
 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA   1506
 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC   1566
 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA   1626
 TTCTCCCTTT TATATTGCAT CTGCTGTTAC CCAGTGAAGC TTACCTAGAG CAATGATCTT   1686
```

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TTTCACGCAT TTGCTTTATT CGAAAAGAGG CTTTTAAAAT GTGCATGTTT AGAAAACAAA 1746
ATTTCTTCAT GGAAATCATA TACATTAGAA AATCACAGTC AGATGTTTAA TCAATCCAAA 1806
AATGTCCACT ATTTCTTATG TCATTCGTTA GTCTACATGT TTCTAAACAT ATAAATGTGA 1866
ATTTAATCAA TTCCTTTCAT AGTTTTATAA TTCTCTGGCA GTTCCTTATG ATAGAGTTTA 1926
TAAAACAGTC CTGTGTAAAC TGCTGGAAGT TCTTCCGGAA TTC 1969

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
 1               5                  10                  15
Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
            20                  25                  30
Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
        35                  40                  45
Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
    50                  55                  60
Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
65                  70                  75                  80
Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
                85                  90                  95
Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
            100                 105                 110
Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
        115                 120                 125
Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
    130                 135                 140
Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 638 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 91...555

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
TGCATTTTGT GCCTTTGCTG GAAGAACCGA CTACAGGTTT GTTCAATTTC TTACAGTCTT    60
GAAAGCGCCA CAAGCAGCAG CTGCTGAGCC  ATG GCT GAA GGG GAA ATC ACC ACC  114
                                  Met Ala Glu Gly Glu Ile Thr Thr
```

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Input Set : N:\Crf3\RULE60\09902460.txt
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```
186                                     1               5
188  TTC ACA GCC CTG ACC GAG AAG TTT AAT CTG CCT CCA GGG AAT TAC AAG     162
189  Phe Thr Ala Leu Thr Glu Lys Phe Asn Leu Pro Pro Gly Asn Tyr Lys
190      10                  15                  20
192  AAG CCC AAA CTC CTC TAC TGT AGC AAC GGG GGC CAC TTC CTG AGG ATC     210
193  Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile
194  25                  30                  35                  40
196  CTT CCG GAT GGC ACA GTG GAT GGG ACA AGG GAC AGG AGC GAC CAG CAC     258
197  Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His
198                  45                  50                  55
200  ATT CAG CTG CAG CTC AGT GCG GAA AGC GTG GGG GAG GTG TAT ATA AAG     306
201  Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys
202              60                  65                  70
204  AGT ACC GAG ACT GGC CAG TAC TTG GCC ATG GAC ACC GAC GGG CTT TTA     354
205  Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu
206          75                  80                  85
208  TAC GGC TCA CAG ACA CCA AAT GAG GAA TGT TTG TTC CTG GAA AGG CTG     402
209  Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu
210      90                  95                  100
212  GAG GAG AAC CAT TAC AAC ACC TAT ATA TCC AAG AAG CAT GCA GAG AAG     450
213  Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys
214  105                 110                 115                 120
216  AAT TGG TTT GTT GGC CTC AAG AAG AAT GGG AGC TGC AAA CGC GGT CCT     498
217  Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro
218                  125                 130                 135
220  CGG ACT CAC TAT GGC CAG AAA GCA ATC TTG TTT CTC CCC CTG CCA GTC     546
221  Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val
222              140                 145                 150
224  TCT TCT GAT TAAAGAGATC TGTTCTGGGT GTTGACCACT CCAGAGAAGT TTCGAGGGG   604
225  Ser Ser Asp
226          155
228  TCCTCACCTG GTTGACCCAA AAATGTTCCC TTGA                               638
230 (2) INFORMATION FOR SEQ ID NO: 4:
232      (i) SEQUENCE CHARACTERISTICS:
233           (A) LENGTH: 155 amino acids
234           (B) TYPE: amino acid
235           (C) STRANDEDNESS: single
236           (D) TOPOLOGY: linear
238     (ii) MOLECULE TYPE: protein
239      (v) FRAGMENT TYPE: internal
241     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
243  Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
244   1               5                  10                  15
245  Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
246              20                  25                  30
247  Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
248          35                  40                  45
249  Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
250      50                  55                  60
```

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```
Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
65                  70                  75                  80
Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
                85                  90                  95
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
            100                 105                 110
Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
        115                 120                 125
Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
    130                 135                 140
Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
AGAATTCAAA TATTCTGAAA TGAGCTGTTG ACAATTAATC ATCGAACTAG TTAACTAGTA   60
CGCAAGTTCA CGTAAAAAGG GTATCACATA TGGTACCTGC AGA                     103
```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
TCTGCAGGTA CCATATGTGA TACCCTTTTT ACGTGAACTT GCGTACTAGT TAACTAGTTC   60
GATGATTAAT TGTCAACAGC TCATTTCAGA ATATTTGAAT TCT                     103
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
GAAATACACC AGTTGG                                                   16
```

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
ACTTGGATCC AAAACAG                                                  17
```

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

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Input Set : N:\Crf3\RULE60\09902460.txt
Output Set: N:\CRF3\12102001\I902460.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]